

Amendments to Specification

Please replace the paragraph beginning at page 22, line 24 – page 23, line 4 with the following rewritten paragraph:

Once aligned, the number of matches is determined by counting the number of positions where an identical nucleotide or amino acid residue is presented in both sequences. The percent sequence identity is determined by dividing the number of matches either by the length of the sequence set forth in the identified sequence, or by an articulated length (for example, 100 consecutive nucleotides or amino acid residues from a sequence set forth in an identified sequence), followed by multiplying the resulting value by 100. For example, a nucleic acid sequence that has 1166 matches when aligned with a test sequence having 1154 nucleotides is 75.0 percent identical to the test sequence (for example, $1166 \div 1554 * 100 = 75.0$). The percent sequence identity value is rounded to the nearest tenth. For example, 75.11, 75.12, 75.13, and 75.14 are rounded down to 75.1, while 75.15, 75.16, 75.17, 75.18, and 75.19 are rounded up to 75.2. The length value will always be an integer. In another example, a target sequence containing a 20-nucleotide region that aligns with 20 consecutive nucleotides from an identified sequence as follows contains a region that shares 75 percent sequence identity to that identified sequence (for example, $15 \div 20 * 100 = 75$).

1 20
Target Sequence: ACGTCGCTACTCTCA
| | | | | | | | | |
Identified Sequence: ACCTGGTGAACCTCCCAGTGA

Please replace the paragraph beginning at page 23, lines 32-34, with the following rewritten paragraph:

FIG. 3A is a nucleotide sequence alignment (SEQ ID NO: 67) between human Rab9A cDNA (Genbank accession no. NM_004251; SEQ ID NO: 67), and simian Rab9A cDNA (Genbank accession no. AY601640; SEQ ID NO: 68). Nonconserved nucleotides are indicated.

Please replace the previous sequence listing with the attached sequence listing.